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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/993,777

DATE: 02/14/2002
 TIME: 09:37:38

Input Set : N:\Crf3\RULE60\09993777.txt
 Output Set: N:\CRF3\02142002\I993777.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Wild, Martha A
 7 Cochran, Mark D
 9 (ii) TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
 10 AND USES THEREOF
 12 (iii) NUMBER OF SEQUENCES: 72
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Cooper & Dunham LLP
 16 (B) STREET: 1185 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: USA
 20 (F) ZIP: 10036
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.25
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/993,777
 C--> 30 (B) FILING DATE: 06-Nov-2001
 31 (C) CLASSIFICATION:
 33 (vii) PRIOR APPLICATION DATA:
 34 (A) APPLICATION NUMBER: 08/468,190
 35 (B) FILING DATE:
 37 (A) APPLICATION NUMBER: US 08/126,597
 38 (B) FILING DATE: 24-SEP-1993
 40 (viii) ATTORNEY/AGENT INFORMATION:
 41 (A) NAME: White, John P
 42 (B) REGISTRATION NUMBER: 28,678
 43 (C) REFERENCE/DOCKET NUMBER: 39116-A
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: (212) 278-0400
 47 (B) TELEFAX: (212) 391-0525
 51 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 13473 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANDEDNESS: single
 57 (D) TOPOLOGY: linear
 59 (ii) MOLECULE TYPE: DNA (genomic)
 61 (iii) HYPOTHETICAL: NO

ENTERED

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64      (ix) FEATURE:
65          (A) NAME/KEY: CDS
66          (B) LOCATION: 10592489
67
68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION: 25754107
71
72      (ix) FEATURE:
73          (A) NAME/KEY: CDS
74          (B) LOCATION: 41134445
75
76      (ix) FEATURE:
77          (A) NAME/KEY: CDS
78          (B) LOCATION: 46095487
79
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION: 56978654
83
84      (ix) FEATURE:
85          (A) NAME/KEY: CDS
86          (B) LOCATION: 987410962
87
88      (ix) FEATURE:
89          (A) NAME/KEY: CDS
90          (B) LOCATION: 1115912658
91
92      (ix) FEATURE:
93          (A) NAME/KEY: CDS
94          (B) LOCATION: 1266513447
95
96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
97      CCCCTGCCCC TAAAGGCGCG CGAGAAAGCT AAGTCCAAAT GTGACGTCGG AGGTCTGACG      60
100 ATGGTCGCCCA ACCTCCAAA TGCTACCCGC CGGCCACGC AACCGGGCT TTTATAAGA      120
102 TGGCGCGCGCA GKAATAAACA CTTACTCATC CGCGTACGCG TTTATTATTG TCAATATTTG      180
104 TGTGGTTATT ATTCTGCTA CCGCCCTGT TTTCTGCAAG CCCTCGCCGC GGCCAGGCC      240
106 ACTATTCCGG CAGCGGCCGC GCACGCGGCG AGCGTCGCCG CTAACGTCGG CGCCGCGGGG      300
108 AGCGGGGGTTT CTTGCACTTA AATAGACTCC CGAGAAAAA TTTTGGCTGC CGTTCCGCAT      360
110 CATCCGAGTC GGAAACACAG TATCGCGCCG AGTCTAGGTTT TACTTTTAAA AACTTTACCG      420
112 TGCCTGTACGG CCAGGGCGTT CTCAGGCTCG AAGGGGCAAG AGTTGTCCAG ACTGATGGGT      480
114 GACTCAGAGA CAGCGTTGTC TTGTCCTCCG TTACCAAAAA TATTCTCACT CTTCTCTCAA      540
116 AATTTTACC TCCGGTTTCG GTAATTAGGA AAGTTTTTGG CGCAGGGAGG TTTAAAGCTG      600
118 CCATGTCATAT GTCAGCGGTA CCCAGCACCC ACAATGGGAA CTCTTTTTCG GCATACGCGC      660
120 CAGATGACAA ATGTGATAAC CCTGGCTCCA AGCCGCTCCA CTCGGGACTT ACTCCAGGGC      720
122 GGTGCGCCCC CTCACGCAAC CGAATCACGG GTCTGCACAT CTTGGGAAGG GAAAACAGCT      780
124 CCGCGGAAAC TTCTCATAGA GATGCCGGGC GCACGATTAC CGATAATGTA CTCGGACGAT      840
126 CGTAACCTGC CATAGTTTTC ACTGCGTGAA CCAATTCTTT CCATCCAGAA TCCGAGAGCT      900
128 CAAATCTAGA ATTAGGTAGT TTGTAGTTCG AATCGACCGC AGAAACTATA GTCACTTTTA      960
130 CAGGCGCCAT CGCGCTCAG ACTCCACCCC GCTATGATGT CAGAAATATA AGCTCTTTAT      1020
132 TTAGCAGAG TCAGGCCAAT ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC      1073
133      Met Arg Phe Arg Arg
134      1 5
136 ATC TGT TCA CGC TCT AGG GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT      1121
137 Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn
138      10 15 20
140 CCG CTT ACC TCA AAA CGC GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA      1169

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141 Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp Ser Phe Ser Arg Thr .
142          25          30          35
144 ATG TCA TTG CGC CCC TAT GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC 1217
145 Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro Thr Ala Glu Gly Val
146          40          45          50
148 GAG CGC CTC GCC GAA CTT GTT AGT ACA ATG ACA GAA CGC GCG GAA 1265
149 Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met Thr Glu Arg Ala Glu
150          55          60          65
152 CCT GTG ACA GAG AAT ACA GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG 1313
153 Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile Pro Pro Ala Asn Glu
154          70          75          80
156 AAC GGG CAG AAC TTC GCA TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA 1361
157 Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu
158          90          95          100
160 AAA GTT GAC GGC TCG CAT ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC 1409
161 Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr
162          105          110          115
164 GCC GGC CCT GTC CCG CTC GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA 1457
165 Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu Lys His Ser Asp Glu
166          120          125          130
168 TTT CTT CAG CAC TTC CGA CTT TTA GAC GAT TTG GTG GAG GGG GCT TAC 1505
169 Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu Val Glu Gly Ala Tyr
170          135          140          145
172 GGG TTT ATC TGC GGC GTC CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA 1553
173 Gly Phe Ile Cys Gly Val Arg Arg Tyr Thr Glu Glu Gln Arg Arg
174          150          155          160
176 AGA GGG GTT AAC AGT ACT AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG 1601
177 Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu
178          170          175          180
180 ATA GCT AAA TAT GTG AAA AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA 1649
181 Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu
182          185          190          195
184 AAT GAA ATT TTG GTT CTC GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG 1697
185 Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His Glu Asn Val Leu Lys
186          200          205          210
188 ATC CAG GAA ATC CTT CGG TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG 1745
189 Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln
190          215          220          225
192 AGG TAT CAG TTC GAC TTG TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC 1793
193 Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp
194          230          235          240
196 TGG AAA GAC AGT CCA ATG CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG 1841
197 Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg Arg Ile Met Lys Gln
198          250          255          260
200 CTC ATG TCA GCG GTC TCG TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG 1889
201 Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys Lys Leu Ile His Arg
202          265          270          275
204 GAC ATC AAA CTC GAA AAT ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG 1937
205 Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys Asp Gly Lys Thr Val

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206          280          285          290          1985
208 CTG GGC GAC TTT GGA ACT GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC
209 Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu Asn Glu Arg Glu Pro
210          295          300          305          2033
212 TTC GAA TAT GGA TGG GTG GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA
213 Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr Asn Ser Pro Glu Ile
214          310          315          320          2081
216 CTC GCC AGG GAT TCG TAC TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA
217 Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly
218          330          335          340          2129
220 GTA GTA TTG CTG GAA ATG GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT
221 Val Val Leu Leu Glu Met Val Ser His Glu Phe Cys Pro Ile Gly Asp
222          345          350          355          2177
224 GGC GGG GGA AAT CCG CAC CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC
225 Gly Gly Gly Asn Pro His Gln Gln Leu Leu Lys Val Ile Asp Ser Leu
226          360          365          370          2225
228 TCA GTT TGT GAT GAA GAG TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT
229 Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn
230          375          380          385          2273
232 TAT TTG CAT TAT GCG AGC ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG
233 Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly His Thr Val Pro Ser
234          390          395          400          2321
236 CTC ATA CGG AAC CTC CAC CTT CCG GCG GAT GTG GAA TAC CTT CTA GTT
237 Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val Glu Tyr Pro Leu Val
238          410          415          420          2369
240 AAA ATG CTT ACT TTT GAC TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA
241 Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro Ser Ala Ala Glu Val
242          425          430          435          2417
244 TTG GCA ATG CCA CTG TTT TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT
245 Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile
246          440          445          450          2465
248 ATT CAT GGA AAA CAT AAA CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG
249 Ile His Gly Lys His Lys Pro Ile Arg Pro Glu Ile Arg Ala Arg Val
250          455          460          465          2516
252 CCA CGG TCC ATG AGT GAA GGT TAATAATAAA GGACGGAGAT AGAGAACTGA
253 Pro Arg Ser Met Ser Glu Gly
254          470          475          2574
256 AGCGTCAGAT TTTTTTAAAA AAATAAATGA TCGAGAACTT ATGATTGTCT TTTCTTGA
257          2622
258 ATG ACC TTG CCC CAT CGA TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC
259 Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
260          5          10          15          2670
w--> 260 1 TGC TCG GTC TTT GTG ATA CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT
262 TGC TCG GTC TTT GTG ATA CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT
263 Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
264          20          25          30          2718
w--> 264 264 AAC AAG ACA ATG TTA CTC TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC
266 AAC AAG ACA ATG TTA CTC TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC
267 Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
268          35          40          45          2766
w--> 268 270 GGA GGC GAC GCA AAT CAC AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT
271 Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile

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Input Set : N:\Cr3\RULE60\09993777.txt
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W-->	272	50	55	60	2814
	275	GGA GCG TTT AGC GCG GCG GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG			
	276	Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr			
W-->	277	65	70	75	80
	279	GAA AGC AGC TCC TCC TCC GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG			2862
	280	Glu Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys			
W-->	281	85	90	95	2910
	283	GAA TTT GGC GGT AAG TGG ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC			
	284	Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala			
W-->	285	100	105	110	2958
	287	GAG GTC CTT TCT CAG GCA TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA			
	288	Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu			
W-->	289	115	120	125	3006
	291	GAT GCG GAG GAG GAG AGA GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA			
	292	Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile			
W-->	293	130	135	140	3054
	295	CAG CCG TTC AAT GCC TGG CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT			
	296	Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp			
W-->	297	145	150	155	3102
	299	TTT ACT CGA GCG CCA ATA GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA			
	300	Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala			
W-->	301	165	170	175	3150
	303	GAG GCG TTG AAA GTA GGG GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA			
	304	Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val			
W-->	305	180	185	190	3198
	307	CGG TTC ACG CGA TCA AAG AAA AGC GTT ACG GTG CCG GAT GCG CAG TCG			
	308	Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser			
W-->	309	195	200	205	3246
	311	TTT TTG GGG GAC TCG TTC TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT			
	312	Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val			
W-->	313	210	215	220	3294
	315	TGC TTA CGA CAG CAC ATA ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC			
	316	Cys Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser			
W-->	317	225	230	235	3342
	319	ATT GTT AAC TGC AAC GAC CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT			
	320	Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe			
W-->	321	245	250	255	3390
	323	CAC TGG AGA GGA ATG GCG GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG			
	324	His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro			
W-->	325	260	265	270	3438
	327	GAG GAG AAT ATT CAA CAC GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG			
	328	Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala			
W-->	329	275	280	285	3486
	331	GGG GCT GGT CTG TTC CTG TGG CCT GCC ATG GCG GCA GCC TTT GAA GAG			
	332	Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu			
W-->	333	290	295	300	3534
	335	CGC GAC AAG CGA CTG TTA AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG			
	336	Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met			
W-->	337	305	310	315	320

VERIFICATION SUMMARY
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:297 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:321 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:333 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:345 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:353 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:357 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:369 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:377 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:401 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:420 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1
L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:457 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:3334 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=55
L:3336 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=55
L:3354 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=56
L:3356 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=56
L:3374 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=57
L:3376 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=57
L:3394 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=58
L:3396 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=58
L:3413 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=59
L:3415 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=59